FORM PTO-1449

INFORMATION DISCLOSURE CITATION IN AN APPLICATION

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Docket Number (Optional)	Application Number
823.0093USQ	10/071,859
Applicant: John R. Desjarlais	
Filing Date: February 6, 2002	Group Art Unit: 2857

U. S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE
/JS/	5,965,408	10/12/99	Short	435	91.1	
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	5,644,048	1/1/97	Yau	536	25.3	
	5,034,506	7/23/91	Summerton et al.	528	391	
	5,235,033	8/10/93	Summerton et al.	528	391	
	4,469,863	9/4/84	Ts'o et al.	536	27	
	5,216,141	6/1/93	Benner	536	27.13	
	5,602,240	2/11/97	De Mesmaeker et al.	536	22.1	
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	WO 97/27213	7/31/97	PCT	C07K	1/04		
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EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP §609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to the applicant.

Substitute Form PTO-1449 (Modified)	U.S. Department of Commerce Patent and Trademark Office	Attorney's Docket No. 16380-003001	Application No. 10/071,859
Information Disclosure Statement by Applicant (Use several sheets if necessary) (37 CFR 1.98(b))		Applicant John R. Desjarlais	
		Filing Date June 8, 2001	Group Art Unit 2857

U.S. Patent Documents

Examiner Initial	Desig. ID	Document Number	Publication Date	Patentee	Class	Subclass	Filing Date If Appropriate
/JS/	AA	US 6,188,965	Feb. 13, 2001	Mayo et al.			
/JS/	AB	US 6,269,312	Jul. 31, 2001	Mayo et al.			
/JS/	AC	US 6,403,312	Jun. 11, 2002	Dahiyat et al.			
/JS/	AD	US 2002/0123846	Sep. 5, 2002	Miller et al.			
	AE						
	AF						
	AG						
	AH						
	AI						
	AJ						
	AK						

Foreign Patent Documents or Published Foreign Patent Applications

Examiner Initial	Desig. ID	Document Number	Publication Date	Country or Patent Office	Class	Subclass	Translation Yes	Translation No
	AL							
	AM							
	AN							
	AO							
	AP							

Other Documents (include Author, Title, Date, and Place of Publication)

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	AQ	
	AR	
	AS	
	AT	

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		Filing Date February 6, 2002	Group Art Unit 1631

Other Documents (include Author, Title, Date, and Place of Publication)		
Examiner Initial	Desig. ID	Document
/JS/	AA	Dahiyat et al. "Automated design of the surface positions of protein helices." *Protein Science.* (1997), 6: 1333-1337.
	AB	Dahiyat et al. "Protein design automation." *Protein Science.* (1996), 5: 895-903.
	AC	Dahiyat et al. "De novo protein design: Fully automated sequence selection." *Science.* Vol. 278, 3 Oct. 1997, 82-87.
	AD	Dahiyat et al. "Probing the role of packing specificity in protein design." *Proc. Natl. Acad. Sci.* USA. Vol. 94, 10172-10177. Scot. 1997.
	AE	Dahiyat et al. "De novo protein design: Towards fully automated sequence selection." *J. Mol. Biol.* (1997)273, 789-796.
	AF	Delarue et al. "The inverse protein folding problem: Self consistent mean field optimisation of a structure specific mutation matrix." *Pac Symp Biocomput.* (1997), 109-121
	AG	Desjarlais et al. "Computer Search Algorithms in protein modification and design." (1998) *Curr Opin Struct Biol.* 8(4), 471-5.
	AH	Desjarlais et al. "De novo design of the hydrophobic cores of proteins." *Protein Science* (1995), 4,2006-18.
	AI	Desjarlais et al. "Side-chain and backbone flexibility in protein core design. *J. Mol. Biol.* (1999), 290(l), 305-18.
	AJ	Desmet et al., "The dead-end elimination theorem and its use in protein side-chain positioning." *Nature.* (1992), 356(9). 539-542.
	AK	Dunbrack et al. "Bayesian statistical analysis of protein side-chain rotamer preferences." *Protein Sci.* (1997) 6(8), 1661-81.
	AL	Eisenberg et al., "Solvation energy in protein folding and binding." *Nature.* 319(6050), 199-203.
	AM	Goldstein . "Efficient rotamer elimination applied to protein side-chains and related spin glasses." *Biophys. J.* (1994) 66(5), 1335-40.
	AN	Gordon. "Energy functions for protein design." *Curr Opin Struct Biol.* (1999), 9(4), 509-1 3.
	AO	Harbury et al. "Repacking protein cores with backbone freedom: structure prediction for coiled coils." *Proc Natl Acad Sci* USA. (1995), 92(18), 8408-12.
	AP	Hellinga. "Rational protein design: combining theory and experiment." *Proc Natl Acad Sci* USA. (1997), 94(19), 10015-17.

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/JS/	AQ	Hellinga et al. "Optimal sequence selection in proteins of known structure by simulated evolution." *Proc Natl Acad Sci USA.* (1994), 91(13), 5803-7.
	AR	Hendsch et al. "Electrostatic interactions in the GCN4 leucine zipper: Substantial contributions arise from intramolecular interactions enhanced on binding." *Protein. Sci.* (1999)8(7), 1381-92.
	AS	Henikoff et al. "Position-based sequence weights." *J. Mol. Biol.* (1994) 243(4), 574-8.
	AT	Holland. "Adaptation in natural and artificial systems." *The MIT Press*, Cambirdge, MA (1992).
	AU	Johnson et al. "Solution structure and dynamics of a designed hydrophobic core variant of ubiquitin." *Structure Fold Des.* (1999), 7(8), 967-76.
	AV	Jorgensen et al. "The OPLS potential functions for proteins. Energy minimizations for crystals of cyclic peptides and crambin." *J. Amer. Chem. Soc.* (1988), 110(6), 1657-1666.
	AW	Koehl et al. "Application of a self-consistent mean field theory to predict protein side-chains conformation and estimate their conformational entropy." *J. Mol. Biol.*, 239(2), 249-75.
	AX	Koehl et al. "Mean-field minimization methods for biological macromolecules." *Curr Opin Struct Biol.*, (1996), 6(2), 222-6.
	AY	Kono et al. "Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry." *Proteins.* (1994), 19(3), 244-255.
	AZ	Kono et al. "Designing the hydrophobic core of Thermus flavus malate dehydrogenase based on side-chain packing." *Protein Eng.* (1998),11(1), 47-52.
	AAA	Kuhlman et al. "Native protein sequences are close to optimal for their structures." *Proc. Natl. Acad. Sci.* USA. (2000), 97(19), 10383-8.
	ABB	Lazar et al. "De novo design of the hydrophobic core of ubiquitin." *Protein Sci.* (1997), 6(6), 1167-78.
	ACC	Lazar et al. "Rotamer strain as a determinant of protein structural specificitv." *Protein Sci.* (1999), 8(12), 2598-610.
	ADD	Lee. "Predicting protein mutant energetics by self-consistent ensemble optimization." *J. Mol. Biol.* (1994), 236(3), 918-39.
	AEE	Micheletti et al. "Design of proteins with hydrophobic and polar amino acids. " *Proteins.* (1998), 32(1), 80-7.
	AFF	Raha et al. "Prediction of amino acid sequence from structure." *Protein Sci.* (2000), 9(6), 1106-19.

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/JS/	AGG	Ranganathan et al. "Structural and functional analysis of the mitotic rotamase Pin1 suggests substrate recognition is phosphorylation dependent." *Cell.* (1997), 89(6), 875-86.
/JS/	AHH	Street et al. "Computational protein design." *Structure Fold Des.* (1999), 7(5), R105-9.
/JS/	AII	Su et al. "Coupling backbone flexibility and amino acid sequence selection in protein design." *Protein Sci.* (1997), 6(8), 1701-7.
/JS/	AJJ	Voigt et al. "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design." *J. Mol. Biol.* (2000), 299(3), 789-803.
/JS/	AKK	Voigt et al. "Computational method to reduce the search space for directed protein evolution." *Proc. Natl. Acad. Sci.* USA. (2001), 98(7). 3778-83.
/JS/	ALL	Weiner et al. "A new force field for molecular mechanical simulation of nucleic acids and proteins." *Journal of the American Chemiccal Society.* (1984). 106(3). 765-84.

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